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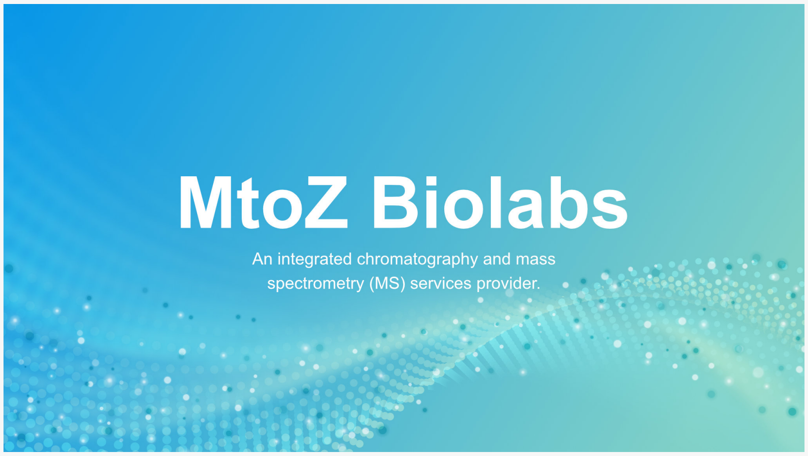
MtoZ Biolabs' Mass Spectrometry-Based Protein Identification Solutions

MS-based protein identification enables comprehensive identification of thousands of proteins.



MtoZ Biolabs, an integrated chromatography and mass spectrometry (MS) services provider.

BOSTON, MA, UNITED STATES, August 27, 2025 /EINPresswire.com/ -- Protein Identification refers to the experimental confirmation of a protein's identity, including its amino acid sequence, biological origin, and potential function. In life sciences, this process is a foundational but essential step, broadly utilized in functional genomics, proteomics, biomarker discovery, disease mechanism studies, drug target validation, and antibody specificity assessment.

While traditional methods like Western blotting and 2D gel electrophoresis remain in use, they suffer from limited sensitivity and narrow proteome coverage. In contrast, mass spectrometry (MS) has emerged as the gold standard for protein analysis, offering unmatched sensitivity, throughput, and specificity. MS-based protein identification enables comprehensive identification of thousands of proteins from complex mixtures, while also providing detailed insights into peptide sequences, post-translational modifications (PTMs), and relative quantification.

MtoZ Biolabs provides mass spectrometry-based protein identification solutions powered by high-resolution instrumentation and intelligent bioinformatics. Our services support a wide range of scientific applications, including disease modeling, protein function elucidation, and large-scale discovery research, enabling researchers to accelerate insights with confidence and precision.

Why Mass Spectrometry for Protein Identification?

1. High Sensitivity and Throughput

Mainstream MS platforms (e.g., Orbitrap Exploris, Q-Exactive, TripleTOF) achieve picomolar (pmol) to attomolar (amol) sensitivity, allowing for trace-level detection of low-abundance proteins. When combined with multidimensional separation techniques—including high-pH reversed-phase LC and SCX—single-run experiments can identify thousands of proteins, facilitating deep coverage of complex proteomes in both discovery and targeted workflows.

2. Effective for Complex and Uncharacterized Samples

Unlike antibody-dependent methods such as ELISA and WB, MS-based protein identification solutions does not require prior knowledge of the protein target. It applies to lysates, plasma, exosomes, cell supernatants, IP complexes, and gel slices, enabling exploration of unknown or highly complex protein mixtures.

3. Simultaneous Detection of PTMs

MS not only confirms protein identities but also characterizes biologically relevant PTMs, including phosphorylation, glycosylation, acetylation, and ubiquitination. This dual capability provides essential insights into protein regulation, signaling pathways, and functional dynamics.

4. High Flexibility and Integration

Our approach integrates seamlessly with co-IP, pull-down assays, and ChIP protocols, enabling cross-platform compatibility. As a result, MS-based protein identification solutions are well-suited for interdisciplinary research spanning molecular biology, translational medicine, and drug development.

MtoZ Biolabs’ Workflow for MS-Based Protein Identification Solutions

MtoZ Biolabs provides a fully integrated, customizable, and modular workflow for MS-based protein identification. Each of the five stages is supported by technical standards and robust quality control.

1. Sample Preparation

We accept a wide range of biological samples—including cell lysates, tissues, serum, plasma, cerebrospinal fluid (CSF), urine, exosomes, and gel bands. Extraction protocols (e.g., SDS, urea, RIPA) are selected based on sample type to maximize protein yield and minimize contaminants. Quality assessment is performed using BCA or Bradford assays, alongside SDS-PAGE for protein integrity verification.

2. Protein Digestion and Peptide Processing

Proteins are digested enzymatically using trypsin or dual enzymes (e.g., Trypsin + Lys-C) to improve sequence coverage. To minimize sample loss and preserve PTMs, we implement advanced preparation techniques such as FASP (Filter-Aided Sample Preparation) and SP3 (Single-Pot Solid-Phase-enhanced Sample Preparation), with protease inhibitors incorporated where PTM retention is required.

3. LC-MS/MS Acquisition

We deploy high-resolution mass spectrometers—including Orbitrap Exploris 480, Q Exactive HF-X, and TripleTOF 6600—combined with Nano-LC systems for enhanced peptide separation. Multiple acquisition modes are available:

(1) DDA (Data-Dependent Acquisition): for comprehensive proteome profiling

(2) DIA (Data-Independent Acquisition): for robust quantification across samples

(3) PRM/SRM: for validating specific protein targets

Single-sample deep scans and batch-mode high-throughput analysis are supported, enabling flexible transitions from global discovery to precise quantitation. This flexibility allows a smooth transition from broad discovery to precise quantitation—key advantages of mass spectrometry-based protein identification solutions.

4. Data Analysis and Functional Annotation

(1) Tools: MaxQuant, Proteome Discoverer, Spectronaut

(2) Databases: UniProt, Swiss-Prot, Human RefSeq; custom databases supported for non-model species

(3) Bioinformatics: GO annotation, KEGG pathway enrichment, Pfam domain prediction, Cytoscape visualization

Applications

1. Disease Mechanism Elucidation

In models of cancer, cardiovascular, and neurodegenerative diseases, mass spectrometry-based protein identification solutions reveal differentially expressed proteins and regulatory nodes, offering insight into disease pathways and potential therapeutic targets.

2. Biomarker Discovery

By profiling proteins in biofluids such as blood and urine and applying statistical models, clinically actionable biomarkers for early detection and precision therapy can be uncovered.

3. Antibody Validation and Protein Interaction Mapping

When paired with co-IP or pull-down assays, MS enables validation of antibody specificity, identification of protein partners, and construction of interaction networks—key to targeted immunological research.

4. Non-Model Organism Proteomics

For plants, insects, and microbes, MtoZ Biolabs offers de novo sequencing and database generation to support proteomic exploration from scratch, expanding MS applications in ecology, agriculture, and biodiversity.

Advantages of MtoZ Biolabs' MS-based protein identification solutions

1. Analysis Platform

We utilize high-resolution mass spectrometers—such as Orbitrap and TripleTOF series—in combination with nano-LC systems, ensuring superior peptide separation, enhanced detection sensitivity, and robust identification performance across diverse sample types.

2. One-Time-Charge

Our one-time, all-inclusive pricing covers all standard procedures—from sample preparation to bioinformatics reporting—ensuring no hidden costs and clear expectations from the outset.

3. High-Data-Quality

Deep data coverage with strict data quality control. An AI-powered bioinformatics platform integrates all protein analysis data, providing clients with a comprehensive data report.

What Could Be Included in the Report?

1. Comprehensive Experimental Details
2. Materials, Instruments, and Methods
3. Total Ion Chromatogram & Quality Control Assessment (project-dependent)
4. Data Analysis, Preprocessing, and Estimation (project-dependent)
5. Bioinformatics Analysis
6. Raw Data

MtoZ Biolabs, an integrated chromatography and mass spectrometry (MS) services provider, provides advanced proteomics, metabolomics, and biopharmaceutical analysis services to researchers in biochemistry, biotechnology, and biopharmaceutical fields. Our ultimate aim is to provide more rapid, high-throughput, and cost-effective analysis, with exceptional data quality and minimal sample consumption.

Whether you’re investigating subtle post-translational modifications, validating novel drug targets, or working with low-yield clinical or environmental samples, high-resolution proteomic data is crucial to driving biological insight and scientific impact. MtoZ Biolabs’ MS-based protein identification solutions empowers researchers to go beyond traditional boundaries—enabling high-throughput, ultra-sensitive, and modification-aware protein analysis with confidence.

Interested in learning more about how our mass spectrometry-based protein identification solutions can enhance your research?

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